

COPY



PCT OPERATIONS

FACSIMILE TRANSMISSION COVER SHEET

DATE: 3/14/02

TO: Dianne Rees

TELEPHONE: (617) 951-3351
FAX NO.: (617) 439-4170

FROM: John Anderson

TELEPHONE: (903) 308-9116
FAX NO.: 703-308-4785 OR 703-305-3230

MESSAGE: Here is the SEQ Error Report.

NUMBER OF PAGES 10 (INCLUDING THIS PAGE)

5630
BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/019,455
Source: Pg 110
Date Processed by STIC: 1/22/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>>, EFS Submission User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/019,455

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) 3,9 missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) 1-2,7-8,13-22,27-28,32-38,42-45 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/019,455

DATE: 01/22/2002
TIME: 10:38:55

pg 1-4

Input Set : A:\56804 Sequence Listing.txt
Output Set: N:\CRF3\01182002\J019455.raw

**Does Not Comply
Corrected Diskette Needed**

**Does Not Comply
Corrected Diskette Needed**

W--> 3 <110> APPLICANT: Takeda Chemical Industries, Ltd.
W--> 4 <120> TITLE OF INVENTION: Novel Polypeptide and its Use
W--> 5 <130> FILE REFERENCE: 2622WO0P
C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/019,455
C--> 6 <141> CURRENT FILING DATE: 2001-10-28
6 <150> PRIOR APPLICATION NUMBER: 1999-06-30
W--> 7 <151> PRIOR FILING DATE: JP 11-186718
W--> 8 <160> NUMBER OF SEQ ID: 48

*This goes next to 1517
This goes on 1507 line*

*Suggestion:
Consult
Sequence Rules*

ERRORED SEQUENCES

E--> 25 <210> SEQ ID NO: 4
E--> 83 <210> SEQ ID NO: 10

173 <210> SEQ ID NO: 19

174 <211> LENGTH: 2019

175 <212> TYPE: DNA

176 <213> ORGANISM: Artificial Sequence

W--> 177 <220> FEATURE:

178 <223> OTHER INFORMATION:

W--> 179 <400> SEQUENCE: 19

E--> 180 accccctggc ccctctgga

364 <210> SEQ ID NO: 36

365 <211> LENGTH: 3936

366 <212> TYPE: DNA

367 <213> ORGANISM: Artificial Sequence

W--> 368 <220> FEATURE:

369 <223> OTHER INFORMATION:

W--> 370 <400> SEQUENCE: 36

E--> 371 cgaattccca ccatggtgtg gtccccagtg ctcctt ← use lower-case letters 36

426 <210> SEQ ID NO: 42

427 <211> LENGTH: 30

428 <212> TYPE: DNA

429 <213> ORGANISM: Artificial Sequence

W--> 430 <220> FEATURE:

431 <223> OTHER INFORMATION:

W--> 432 <400> SEQUENCE: 42

E--> 433 caccaggatg agatgggaat tgtgggttat ← use lower-case

434 <210> SEQ ID NO: 43

435 <211> LENGTH: 30

436 <212> TYPE: DNA

437 <213> ORGANISM: Artificial Sequence

W--> 438 <220> FEATURE:

The types of errors shown exist throughout the Sequence Listing. Please check all sequences for similar errors.

2019

*see item 11
on Ena Summary
sheet*

item 11

item 11

*30 ← insert cumulative base
total at right margin
of each line*

*item 11
(see p. 2)*

DATE: 01/22/2002

TIME: 10:38:55

Output Set: N:\CRF3\01182002\J019455.raw

Deliti

10/019,455 3

use lower-case letters for nucleotides, when using
new sequence
rules format

<400> 2

CAGCGTGTGT ACCAGGAAGC TACCAA

26

<210> 4

where is
sequence 3?

If intentionally
skipped, use
the format shown
in item 80 on Ena
summary sheet

10/019,455 4

↓ use lower-case letters

<400> 8

AACTTGGTGA AGGAGCAGCG TGTA

24

<210> 10

→ where is
sequence 9?

VERIFICATION SUMMARY

DATE: 01/22/2002

PATENT APPLICATION: US/10/019,455

TIME: 10:38:56

Input Set : A:\56804 Sequence Listing.txt

Output Set: N:\CRF3\01182002\J019455.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:7 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:9 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <220> field identifier
L:15 M:283 W: Missing Blank Line separator, <400> field identifier
L:16 M:112 C: (48) String data converted to lower case,
L:21 M:283 W: Missing Blank Line separator, <220> field identifier
L:23 M:283 W: Missing Blank Line separator, <400> field identifier
L:24 M:112 C: (48) String data converted to lower case,
L:25 M:214 E: (33) Seq.# missing, SEQ ID NO:3
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:30 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=4
L:41 M:283 W: Missing Blank Line separator, <400> field identifier
L:50 M:283 W: Missing Blank Line separator, <400> field identifier
L:71 M:283 W: Missing Blank Line separator, <220> field identifier
L:73 M:283 W: Missing Blank Line separator, <400> field identifier
L:74 M:112 C: (48) String data converted to lower case,
L:79 M:283 W: Missing Blank Line separator, <220> field identifier
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:82 M:112 C: (48) String data converted to lower case,
L:83 M:214 E: (33) Seq.# missing, SEQ ID NO:9
L:87 M:283 W: Missing Blank Line separator, <400> field identifier
L:88 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=10
L:99 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:283 W: Missing Blank Line separator, <400> field identifier
L:129 M:283 W: Missing Blank Line separator, <220> field identifier
L:131 M:283 W: Missing Blank Line separator, <400> field identifier
L:132 M:112 C: (48) String data converted to lower case,
L:137 M:283 W: Missing Blank Line separator, <220> field identifier
L:139 M:283 W: Missing Blank Line separator, <400> field identifier
L:140 M:112 C: (48) String data converted to lower case,
L:145 M:283 W: Missing Blank Line separator, <220> field identifier
L:147 M:283 W: Missing Blank Line separator, <400> field identifier
L:148 M:112 C: (48) String data converted to lower case,
L:153 M:283 W: Missing Blank Line separator, <220> field identifier
L:155 M:283 W: Missing Blank Line separator, <400> field identifier
L:156 M:112 C: (48) String data converted to lower case,
L:161 M:283 W: Missing Blank Line separator, <220> field identifier
L:163 M:283 W: Missing Blank Line separator, <400> field identifier
L:164 M:112 C: (48) String data converted to lower case,
~~L:169 M:283 W: Missing Blank Line separator, <220> field identifier~~
L:171 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY

DATE: 01/22/2002

PATENT APPLICATION: US/10/019,455

TIME: 10:38:56

Input Set : A:\56804 Sequence Listing.txt

Output Set: N:\CRF3\01182002\J019455.raw

L:172 M:112 C: (48) String data converted to lower case,
L:177 M:283 W: Missing Blank Line separator, <220> field identifier
L:179 M:283 W: Missing Blank Line separator, <400> field identifier
L:180 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:19 SEQ:19
M:112 Repeated in SeqNo=19
L:180 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:19 SEQ:19
L:185 M:283 W: Missing Blank Line separator, <220> field identifier
L:187 M:283 W: Missing Blank Line separator, <400> field identifier
L:188 M:112 C: (48) String data converted to lower case,
L:193 M:283 W: Missing Blank Line separator, <220> field identifier
L:195 M:283 W: Missing Blank Line separator, <400> field identifier
L:196 M:112 C: (48) String data converted to lower case,
L:201 M:283 W: Missing Blank Line separator, <220> field identifier
L:203 M:283 W: Missing Blank Line separator, <400> field identifier
L:204 M:112 C: (48) String data converted to lower case,
L:209 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=23
L:220 M:283 W: Missing Blank Line separator, <400> field identifier
L:239 M:283 W: Missing Blank Line separator, <400> field identifier
L:240 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=25
L:250 M:283 W: Missing Blank Line separator, <400> field identifier
L:269 M:283 W: Missing Blank Line separator, <220> field identifier
L:271 M:283 W: Missing Blank Line separator, <400> field identifier
L:272 M:112 C: (48) String data converted to lower case,
L:277 M:283 W: Missing Blank Line separator, <220> field identifier
L:279 M:283 W: Missing Blank Line separator, <400> field identifier
L:280 M:112 C: (48) String data converted to lower case,
L:285 M:283 W: Missing Blank Line separator, <400> field identifier
L:286 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=29
L:306 M:283 W: Missing Blank Line separator, <400> field identifier
L:307 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=30
L:327 M:283 W: Missing Blank Line separator, <400> field identifier
L:336 M:283 W: Missing Blank Line separator, <220> field identifier
L:339 M:112 C: (48) String data converted to lower case,
L:347 M:112 C: (48) String data converted to lower case,
L:355 M:112 C: (48) String data converted to lower case,
L:363 M:112 C: (48) String data converted to lower case,
L:371 M:112 C: (48) String data converted to lower case,
L:371 M:252 E: No. of Seq. differs, <211>LENGTH:Input:39 Found:36 SEQ:36
L:379 M:112 C: (48) String data converted to lower case,
L:387 M:112 C: (48) String data converted to lower case,
L:410 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=40
L:420 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=41

VERIFICATION SUMMARY

DATE: 01/22/2002

PATENT APPLICATION: US/10/019,455

TIME: 10:38:56

Input Set : A:\56804 Sequence Listing.txt

Output Set: N:\CRF3\01182002\J019455.raw

L:433 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:42
M:112 Repeated in SeqNo=42
L:441 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:43
M:112 Repeated in SeqNo=43
L:449 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:44
M:112 Repeated in SeqNo=44
L:457 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:45
M:112 Repeated in SeqNo=45
L:463 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=46
L:496 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=48
L:529 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:50